

**REMARKS**

Entry of the above amendment prior to examination is respectfully requested.

Attached hereto is a marked-up version of the changes made to the specification and claims. The attached pages are captioned "**Version with Markings to Show Changes Made.**"

**I. Amendments**

The specification has been amended in accordance with 37 C.F.R. §1.821 through 1.825 to add the Sequence Listing.

The specification and claims have been amended in accordance with 37 C.F.R. §1.821(d) to add SEQ ID NO:s.

The specification has further been amended to remove embedded hyperlinks in accord with MPEP §608.01.

No new matter is introduced by way of these amendments.

If in the opinion of the Examiner a telephone conference would expedite the prosecution of the subject application, the Examiner is encouraged to call the undersigned at (650) 846-7615.

Respectfully submitted,

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**Version with Markings to Show Changes Made**

**In the specification:**

On page 7, please replace the paragraph starting on line 5 with the following:

Figure 2 shows the predicted amino acid sequence (SEQ ID NO:2) and signal sequence (SEQ ID NO:3) based on the nucleotide sequence provided in Figure 1 (SEQ ID NO:1), wherein the signal sequence is indicated as bolded.

On page 19, please replace the paragraph starting on line 3 with the following:

A Basic BLASTN search (<http://www.ncbi.nlm.nih.gov/BLAST>) of the non-redundant nucleic acid sequence database was conducted on September 12, 2001, with the *egl6* gene sequence presented in Figure 1 (SEQ ID NO:1), indicated no sequences producing significant alignments (i.e. with an E value of less than  $10^{-5}$ ).

Part of the *egl6* sequence presented in Figure 1 (SEQ ID NO:1) is identical to parts of the sequences of *Trichoderma reesei* ESTs disclosed as SEQ ID NO:7511 and SEQ ID NO:7641 and annotated as endoglucanases in patent application WO 0056762.

On page 24, please replace the paragraph starting on line 8 with the following:

Figure 2 shows the predicted amino acid sequence (SEQ ID NO:2) of an exemplary EGVI polypeptide based on the nucleotide sequence provided in Figure 1 (SEQ ID NO:1). The predicted molecular weight of the encoded EGVI polypeptide is 87.1kDa. A predicted signal peptide of 19 amino acids precedes the mature amino terminus of EGVI as provided in the figure suggesting that the EGVI polypeptide is secreted (Nielsen, H., Engelbrecht, J., Brunak, S., von Heijne, G., Protein Engineering, 10:1-6, 1997). The last 35 amino acids of the sequence (SEQ ID NO:2) has up to 65% identity with the cellulose binding domains present on many fungal secreted cellulases and hemicellulases (Tomme, P., Warren, R.A., Miller, R.C., Jr., Kilburn, D.G. & Gilkes, N.R. (1995) in Enzymatic Degradation of Insoluble Polysaccharides (Saddler, J.N. & Penner, M., eds.), Cellulose-binding domains: classification and properties. pp. 142-163, American Chemical Society, Washington). The amino acids from approximately residue number 744 to approximately residue number 801 have the characteristics of a serine- and threonine-rich linker region which is generally found between the cellulose binding domain and the catalytic region of fungal enzymes having a cellulose binding domain.

On page 24, please replace the paragraph starting on line 24 with the following:

A Basic BLASTP search ([\[http://www.ncbi.nlm.nih.gov/BLAST\]](http://www.ncbi.nlm.nih.gov/BLAST)) of the non-redundant protein database, conducted on September 12, 2001 with the EGVI amino acid sequence indicated 51% identity with GenBank Accession Number AB015511 (avicellase III of *Aspergillus aculeatus*), 49% sequence identity to GenBank Accession Number AJ292929 (CEL6 protein of *Agaricus bisporus*), 39% sequence identity to GenBank Accession Number AE007608 (probable secreted sialidase of *Clostridium acetabutylicum*), and 40% sequence identity to GenBank Accession Number AL031515 (probable secreted cellulase of *Streptomyces coelicolor*). These sequence similarities indicate that EGVI is a member of glycosyl hydrolase family 74 (Henrissat, B. and Bairoch, A. (1993) *Biochem. J.* 293:781-788).

On page 29, please replace the paragraph starting on line 11 with the following:

Preferred culture conditions for a given filamentous fungus may be found in the scientific literature and/or from the source of the fungi such as the American Type Culture Collection (ATCC; "<http://www.atcc.org/>"). After fungal growth has been established, the cells are exposed to conditions effective to cause or permit the over expression of EGVI.

On page 37, please replace the paragraph starting on line 29 with the following:

Exemplary computer programs which can be used to determine identity between two sequences include, but are not limited to, the suite of BLAST programs, *e.g.*, BLASTN, BLASTX, and TBLASTX, BLASTP and TBLASTN, publicly available on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. See also, Altschul, *et al.*, 1990 and Altschul, *et al.*, 1997.

In the claims:

2. An isolated polynucleotide selected from the group consisting of:
  - (a) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGVI polypeptide having at least 85% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
  - (b) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGVI polypeptide having at least 90% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);

- (c) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGV1 polypeptide having at least 95% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
  - (d) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGV1 polypeptide having the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
  - (e) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGV1 polypeptide having at least 95% sequence identity to the amino acid sequence presented as SEQ ID NO:2;
  - (f) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGV1 polypeptide having the amino acid sequence presented as SEQ ID NO:2;
  - (g) a nucleic acid sequence presented as SEQ ID NO:4, or the complement thereof; and
  - (h) a nucleic acid sequence that hybridizes, under high stringency conditions to the sequence presented as SEQ ID NO:4, or the complement or a fragment thereof, wherein said isolated polynucleotide encodes a polypeptide having the biological activity of an endoglucanase.
8. An expression construct including a polynucleotide sequence (i) having at least 85% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2), or (ii) being capable of hybridizing to a probe derived from the nucleotide sequence disclosed in Figure 2 (SEQ ID NO:2) under conditions of intermediate to high stringency, or (iii) being complementary to a nucleotide sequence having at least 85% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2).
18. A substantially purified EGV1 polypeptide with the biological activity of an endoglucanase, comprising a sequence selected from the group consisting of:
- (a) an amino acid sequence having at least 85% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
  - (b) an amino acid sequence having at least 90% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
  - (c) an amino acid sequence having at least 95% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);

- (d) an amino acid sequence presented in Figure 2 (SEQ ID NO:2);
- (e) an amino acid sequence having at least 95% sequence identity to the amino acid sequence presented as SEQ ID NO:2;
- (f) an amino acid sequence presented as SEQ ID NO:2;
- (g) a substantially purified biologically active fragment of the amino acid sequence presented as SEQ ID NO:2.

25. A detergent composition, said composition comprising a polypeptide selected from the group consisting of:

- (a) an amino acid sequence having at least 85% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
- (b) an amino acid sequence having at least 90% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
- (c) an amino acid sequence having at least 95% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
- (d) an amino acid sequence presented in Figure 2 (SEQ ID NO:2);
- (e) an amino acid sequence having at least 95% sequence identity to the amino acid sequence presented as SEQ ID NO:2;
- (f) an amino acid sequence presented as SEQ ID NO:2;
- (g) a substantially purified biologically active fragment of the amino acid sequence presented as SEQ ID NO:2.